```
10                            30                            50                            70
gaattccggcgagtgaggcgctgacagggactcgcgggggcatcttgcacagacccctggaccacgccgccatcgcagcctccag
90                            110                           130                           150                           170
cccagtcctctctctgccgcttctcctcgccatggaggccgccgaccgccgtccgcgggcttcgagcagcggccgggccgggct
190                           210                           230                           250
gaccccatgtgggccgagagcccggtcctgaggcggagctgccgtgcgcgtcccccgcggtcccgccccagcgccgggctcggt
270                           290                           310                           330
cagcatggattcctggttcattcttgtcctgtttggcagtggtctaatacatgttagtgccaacaatgctactacagtttcccc
   M  D  S  W  F  I  L  V  L  F  G  S  G  L  I  H  V  S  A  N  N  A  T  T  V  S  P
350                           370                           390                           410
ttctttaggaacgacaagattaattaaaacatcaacaacagaattggctaaggaagagaataaaacctcaaattcaacctcttc
 S  L  G  T  T  R  L  I  K  T  S  T  T  E  L  A  K  E  E  N  K  T  S  N  S  T  S  S
430                           450                           470                           490
agtaatttctctttctgtggcaccaacattcagcccaaacctgactctggagcccacctatgtgactactgttaattcttcaca
 V  I  S  L  S  V  A  P  T  F  S  P  N  L  T  L  E  P  T  Y  V  T  T  V  N  S  S  H
510                           530                           550                           570                           590
ctctgacaatgggaccaggagggcagccagcacggaatctggaggcactaccatttccccgaacggaagctggcttattgagaa
 S  D  N  G  T  R  R  A  A  S  T  E  S  G  G  T  T  I  S  P  N  G  S  W  L  I  E  N
610                           630                           650                           670
ccagttcacggatgccataacagaaccctgggagggggaactccagcactgcagcaaccactccagaaaccttcccccggcaga
 Q  F  T  D  A  I  T  E  P  W  E  G  N  S  S  T  A  A  T  T  P  E  T  F  P  P  A  D
690                           710                           730                           750
tgagacaccaattattgcggtgatggtggccctgtcctctctgctagtaatcgtgtttattatcatagttctgtacatgttaag
 E  T  P  I  I  A  V  M  V  A  L  S  S  L  L  V  I  V  F  I  I  I  V  L  Y  M  L  R
770                           790                           810                           830
gtttaagaaatacaagcaagctgggagtcattccaactctttccgcctgtcaaatggccgcacggaggatgtggagccccaaag
 F  K  K  Y  K  Q  A  G  S  H  S  N  S  F  R  L  S  N  G  R  T  E  D  V  E  P  Q  S
```

FIG.1A

```
850                870                890                910
tgtaccacttctggccaggtccccgagcaccaacaggaagtacccaccactgcctgtggacaagctggaagaggagattaaccg
 V  P  L  L  A  R  S  P  S  T  N  R  K  Y  P  P  L  P  V  D  K  L  E  E  E  I  N  R
930                950                970                990                1010
gagaatggctgatgacaataagctcttcagagaagaattcaacgctctccctgcttgtcctatccaggccacctgtgaggctgc
 R  M  A  D  D  N  K  L  F  R  E  E  F  N  A  L  P  A  C  P  I  Q  A  T  C  E  A  A
            1030               1050               1070               1090
ctccaaggaagaaaacaaggaaaaaaaccgctatgtaaacatcctgccctatgaccactctagagtgcacctgacacctgttg
 S  K  E  E  N  K  E [K  N  R  Y  V  N  I  L  P  Y  D  H  S  R  V  H  L  T  P  V  E
          1110               1130               1150               1170
aaggggtcccagattctgattacatcaacgcttcattcattaatggctaccaggaaaagaacaaattcatcgctgcacaaggac
  G  V  P  D  S  D  Y  I  N  A  S  F  I  N  G  Y  Q  E  K  N  K  F  I  A  A  Q  G  P
       1190               1210               1230               1250
caaaagaagaaacagtgaatgacttctggagaatgatatgggaacaaaacacagctactattgtcatggtgaccaacctgaagg
  K  E  E  T  V  N  D  F  W  R  M  I  W  E  Q  N  T  A  T  I  V  M  V  T  N  L  K  E
    1270               1290               1310               1330
agagaaaggagtgtaaatgtgcccaatactggccagaccaaggctgctggacctatgggaatgtccgtgtgtctgtcgaggatg
  R  K  E  C  K  C  A  Q  Y  W  P  D  Q  G  C  W  T  Y  G  N  V  R  V  S  V  E  D  V
1350               1370               1390               1410               1430
tgactgttctggtggactacacagtacggaaattctcgatccagcaggtgggcgacgtgaccaacaggaaaccacagcgcctcat
  T  V  L  V  D  Y  T  V  R  K  F  S  I  Q  Q  V  G  D  V  T  N  R  K  P  Q  R  L  I
             1450               1470               1490               1510
cactcagttccacttcaccagctggccagactttggggtgcctttcacccccaattggcatgctcaagttcctcaagaaggtgaag
 T  Q  F  H  F  T  S  W  P  D  F  G  V  P  F  T  P  I  G  M  L  K  F  L  K  K  V  K
        1530               1550               1570               1590
gcctgtaaccctcagtacgcaggggctatcgtggtccactgcagtgcaggtgtagggcgcactggcacctttgttgtcatcgatg
A  C  N  P  Q  Y  A  G  A  I  V  V  H  C  S  A  G  V  G  R  T  G  T  F  V  V  I  D  A
```

FIG.1B

```
 1610                          1630                          1650                          1670
ccatgctggacatgatgcattcggagcgcaaagtggatgtatatgggtttgtgagccggatccgggcccagcgctgccagatggta
  M  L  D  M  M  H  S  E  R  K  V  D  V  Y  G  F  V  S  R  I  R  A  Q  R  C  Q  M  V
1690                          1710                          1730                          1750                          1770
cagacagacatgcagtacgtcttcatataccaggcccttctggagcattatctgtatggggacacagaactggaagtgacttctc
Q  T  D  M  Q  Y  V  F  I  Y] Q  A  L  L  E  H  Y  L  Y  G  D  T  E  L  E  V  T  S  L
                1790                          1810                          1830                          1850
tagaaacccacctacaaaaaatttataacaagatcccagggactagcaacaacgggttagaggaggagtttaagaaattaacttc
  E  T  H  L  Q  K  I  Y  N  K  I  P  G  T  S  N  N  G  L  E  E  E  F  K  K  L  T  S
       1870                          1890                          1910                          1930
aatcaaaatccagaatgacaagatgcgcacgggaaaccttccagccaacatgaagaagaaccgggttttacagatcattccatat
 I  K  I  Q  N  D  K  M  R  T  G  N  L  P  A  N  M  K [K  N  R  V  L  Q  I  I  P  Y
    1950                          1970                          1990                          2010
gaatttaacagagtgatcattccagtcaaacgaggcgaagagaacacagactatgtgaacgcatccttcattgatggataccggc
E  F  N  R  V  I  I  P  V  K  R  G  E  E  N  T  D  Y  V  N  A  S  F  I  D  G  Y  R  Q
2030                          2050                          2070                          2090                          2110
agaaagactcctacattgccagccagggccctcttctccacacgattgaggacttctggcgaatgatctgggagtggaagtcctg
  K  D  S  Y  I  A  S  Q  G  P  L  L  H  T  I  E  D  F  W  R  M  I  W  E  W  K  S  C
               2130                          2150                          2170                          2190
ttctatcgtaatgctgacagaactggaagagagaggccaggagaagtgtgcccagtactggccatctgatggcctggtgtcctac
 S  I  V  M  L  T  E  L  E  E  R  G  Q  E  K  C  A  Q  Y  W  P  S  D  G  L  V  S  Y
       2210                          2230                          2250                          2270
ggagacatcacagttgagctgaagaaggaggaggaatgtgaaagctacactgtccgagacctcctggtcaccaacaccagggaga   II
G  D  I  T  V  E  L  K  K  E  E  E  C  E  S  Y  T  V  R  D  L  L  V  T  N  T  R  E  N
```

FIG.1C

```
2290                2310                2330                2350
acaagagtcggcaaatccggcagttccacttccacggctggcctgaggtgggcatccccagcgacggcaagggcatgatcaacat
 K  S  R  Q  I  R  Q  F  H  F  H  G  W  P  E  V  G  I  P  S  D  G  K  G  M  I  N  I
2370                2390                2410                2430                2450
cattgcagcagtgcagaagcagcagcagcagtcggggaaccatcccatcactgtgcactgcagtgccggggcaggacggacagga
 I  A  A  V  Q  K  Q  Q  Q  S  G  N  H  P  I  T  V  H  C  S  A  G  A  G  R  T  G

          2470                2490                2510                2530
accttctgtgccttgagcacagtcctggaacgtgtgaaagcagaaggaattttagatgtcttccaaactgtcaagagcctgcggc
 T  F  C  A  L  S  T  V  L  E  R  V  K  A  E  G  I  L  D  V  F  Q  T  V  K  S  L  R  L

          2550                2570                2590                2610
tgcagaggccacacatggtccagacactggaacagtatgaattctgctacaaggtggtacaggaatacattgacgcctttcaga
 Q  R  P  H  M  V  Q  T  L  E  Q  Y  E  F  C  Y] K  V  V  Q  E  Y  I  D  A  F  S  D
     2630                2650                2670                2690
ttatgccaacttcaagtgacaggtgacaaggcccacagacaggagaattgcctttaatattttgtaatattctgtttttgttaat
 Y  A  N  F  K -.
2710                2730                2750                2770                2790
atacccaaaattgtatatatcttataactgttttagaaatggcacataggcttctattacctgttagatggagattttgtatgta
               2810                2830                2850                2870
aatgtgttagcactgatagtcctttccagtgtttattgggaaattaatagtgtgatatttgggttgatataatgaattc
```

FIG.1D

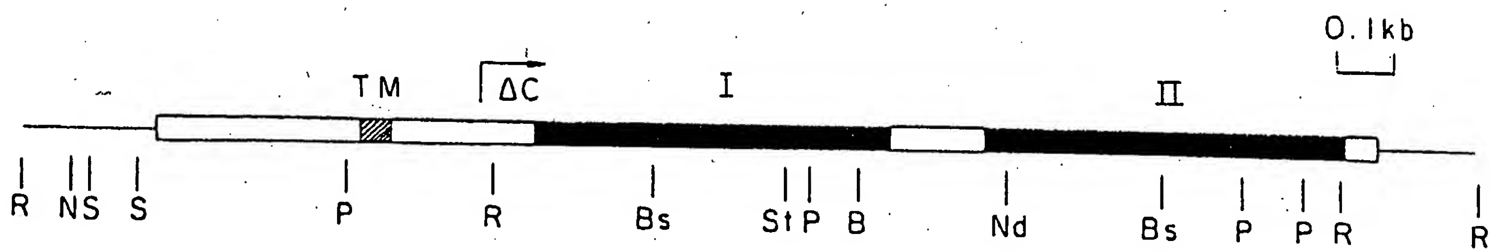


FIG.1E

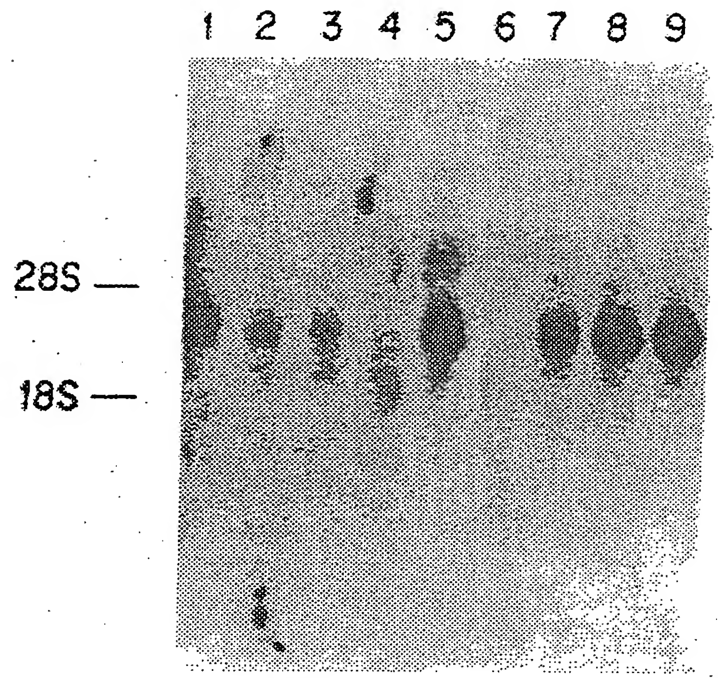


FIG. 2

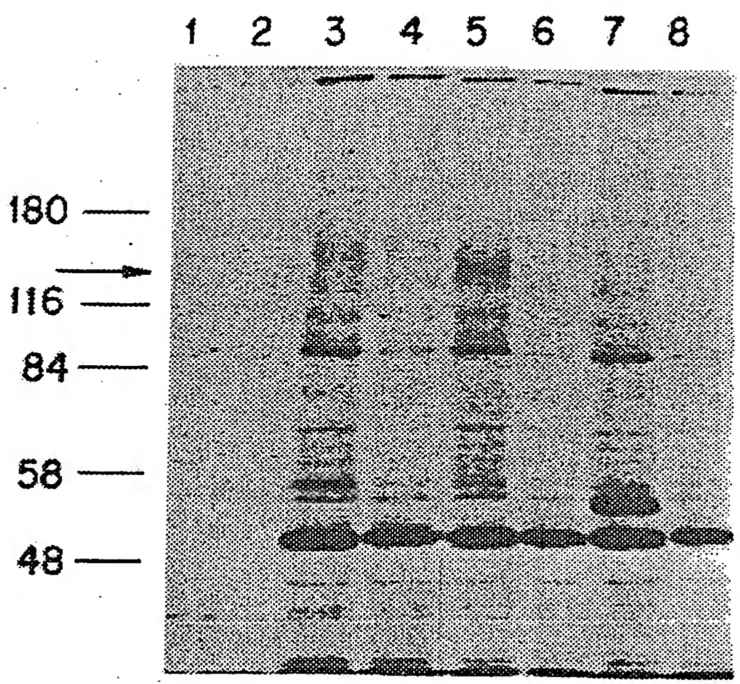


FIG. 3

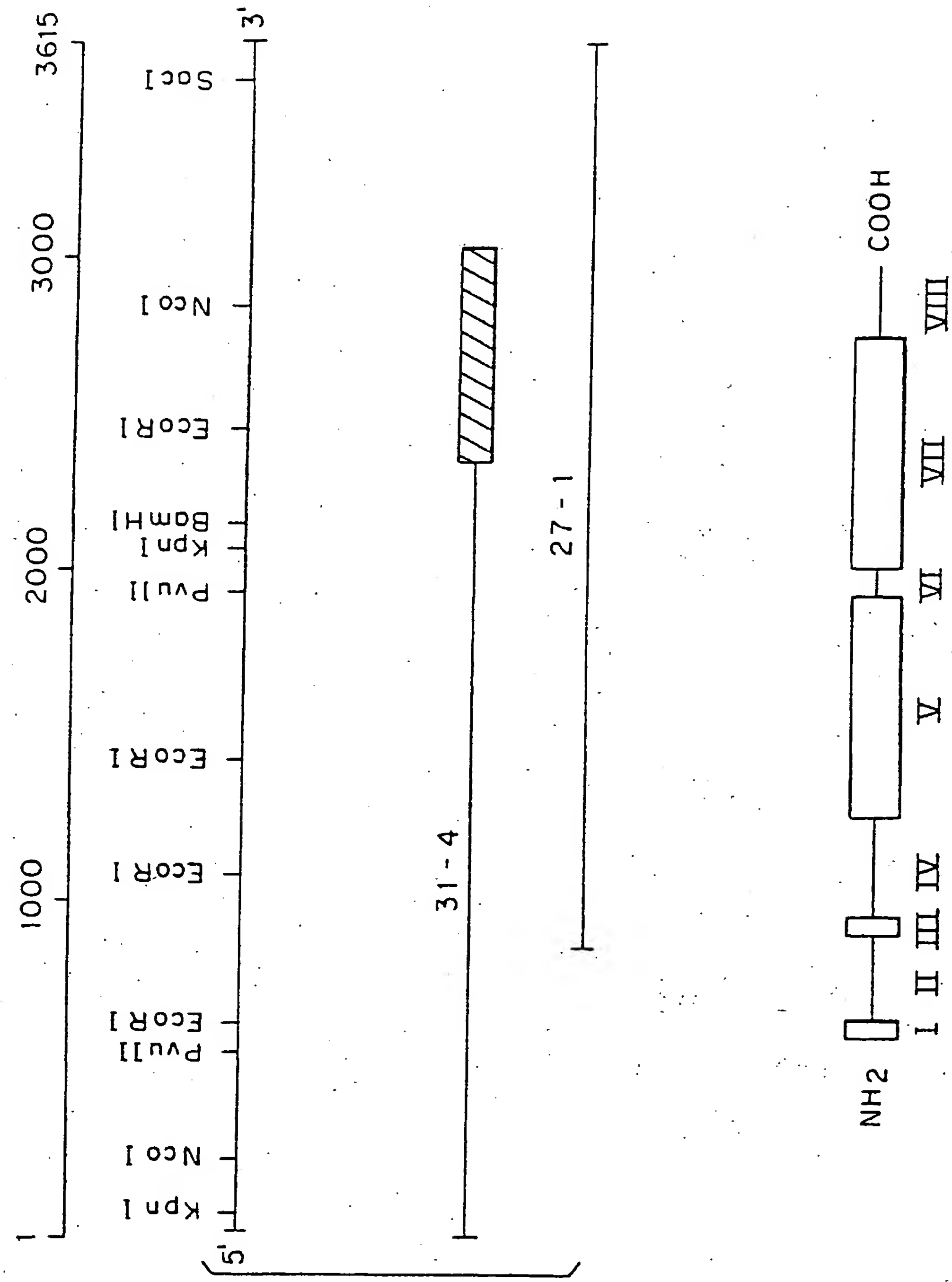


FIG.4A

FIG.4B

FIG.4C

```
        I
1 MDSWFILVLLGSGLICVS ANNATTVAPSVGITRLINSSTAEPVKEEAKTSNPTSSLTSLSVAPTFSP  68
2          F    H          S L T   KT  T LA   N   S   VI                68
1 NITLGPTYLTTVNSSDSDNGTTRTASTNSIGITISPNGTWLPDNQFTDARTEPWEGNSSTAAT TPETFP 136
2  L  E  V     H     R A   E G T      S  IE      I                      136
                          III
1 PSGNSDSKDRRDETPIIAVMVALSSLLVIVFIIIVLYMLRFKKYKQAGSHSNSFRLSNGRTEDVEPQS 204
2 A-----------                                                         195
1 VPLLARSPSTNRKYPPLPVDKLEEEINRRMADDNKLFREEFNALPACPIQATCEAASKEENKEKNRYV 272
2                                                                      263
1 NILPYDHSRVHLTPVEGVPDSDYINASFINGYQEKNKFIAAQGPKEETVNDFWRMIWEQNTATIVMVT 340
2                                     V                                331
1 NLKERKECKCAQYWPDQGCWTYGNIRVSVEDVTVLVDYTVRKFCIQQVGDMTNRKPQRLITQFHFTSW 408
2                              V                S        V             399
1 PDFGVPFTPIGMLKFLKKVKACNPQYAGAIVVHCSAGVGRTGTFVVIDAMLDMMHTERKVDVYGFVSR 476
2                                                         S            467
1 IRAQRCQMVQTDMQYVFIYQALLEHYLYGDTELEVTSLETHLQKIYNKIPGTSNNGLEEEFKKLTSIK 544
2                                                                      535
1 IQNDKMRTGNLPANMKKNRVLQIIPYEFNRVIIPVKRGEENTDYVNASFIDGYRQKDSYIASQGPLLH 612
2                                   VII                                603
1 TIEDFWRMIWEWKSCSIVMLTELEERGQEKCAQYWPSDGLVSYGDITVELKKEEECESYTVRDLLVTN 680
2                                                                      671
1 TRENKSRQIRQFHFHGWPEVGIPSDGKGMISIIAAVQKQQQQSGNHPITVHCSAGAGRTGTFCALSTV 748
2                                N                                     739
1 LERVKAEGILDVFQTVKSLRLQRPHMVQTLEQYEFCYKVVQEYIDAFSDYANFK               802
2                                                                      793
```

FIG.4D

```
                 10        20         30        40
LCA          NqnKNRYVdILPYDynRVeL  sEinGdagSnYINASyIdGfkEprKyIAA
RPTPase α    NKeKNRYVNILPYDHSRVhLtpvE  GvpdSDYINASfInGYqEknKfIAA
RPTPase β    NKHKNRYINIvAYDHSRVKLaqLaeKDgKItDYINANYVDGYNrpKAYIAA
RPTPase γ    NKHKNRYINIIAYDHSRVKLrpLpgKDsKhsDYINANYVDGYNkaKAYIAt

CON          NkhKNRY-nII-YDhsRVkL—l—k—k-sdYINA-y-dGynepk-yIAa

             50        60        70        80        90
LCA          QGPrdETVdDFWRMIWEQkatvIVMVTrceEgnrnKCAeYWPsMeegTra
RPTPase α    QGPkeETVnDFWRMIWEQNtatIVMVTNLkErkecKCAQYWPdqGewTYG
RPTPase β    QGPLKSTaEDFWRMIWEhNvevIVMITNLVEKGRRKCDQYWPadGSEEYG
RPTPase γ    QGPLKSTfEDFWRMIWEqNtgiIVMITNLVEKGRRKCDQYWPtenSEEYG

CON          QGPlk-TveDFWRMIWEqnt-vIVM-TnlvEkgrrKC-qYWP—gse-yg

             100       110       120                 130
LCA          fgdVvVkinqhkrcpDYiiqKI      nIvn     kkekatgRevThiq
RPTPase α    NirVsVedVtVLv  DYTVRKFc     IqqvGd   mtnRkpqRIiTQfH
RPTPase β    NfIVTqKSVqVLA  yYTVRnFtIRNTKIKK Gs   qKGRpsgRVVTQYH
RPTPase γ    NiiVTIKStkihAc  YTVRrFsiRNTKvKK GqkgnpKGRqneRVViQYH

CON          ni-Vtvk-v-vla—dYtvrkf—rntki-k-g-k——kgr—gRvvtqyh
```

FIG.5A

```
               140       150       160       170       180       190
LCA            FTSWPDhGVPedPhIILKIrrrVnAfsnffsGpIVVHCSAGVGRTGTyigID
RPTPase α      FTSWPDfGVPftPigmLKFIkKVkAcnpqyaGaIVVHCSAGVGRTGTfvVID
RPTPase β      YTQWPDMGVPEYsLPVLTFVRKaayAkrhavGPVVVHCSAGVGRTGTYIVID
RPTPase γ      YTQWPDMGVPEYaLPVLTFVRrssaArmpetGPVIVHCSAGVGRTGTYIViD
CON            -T-WPDmGVPeyplpvL-fvr-v-aa-----Gp-vVHCSAGVGRTGTyiviD

                         200       210       220       230
LCA            AMLegleaEnKVDVYGyVvkIRrQRCIMVQveaQYiIIhQALvE
RPTPase α      AMLdmmhtErKVDVYGFVsrIRaQRCqMVQTdmQYVFIyQALIE
RPTPase β      SMLQQIqhEgTVNifGFLKHIRsQRNYLVQTEEQYVFIHDtLvE
RPTPase γ      SMLQQIkdksTVNvIGFLKHIRtQRNYLVQTEEQYiFIHDaLIE
CON            -MLqqi--e--V-vyGf-khiR-QR-y-VQteeQY-fIh-aL-E
```

FIG.5B

```
                 10        20        30        40
LCA          NksKNRnsnvIPYdyNRVpIkheIemskesehdsdessdddsdsEEpskY
RPTPase α    NmkKNRvIqIIPYEfNRViIpvkr                     GEEnTDY
RPTPase β    NrEKNRtSSIIPvERsRVGIssLs                     GE GTDY
RPTPase γ    NkEKNRnSSvvPsERaRVGIapLp                     GmkGTDY

CON          NkeKNRnss-iPyernRVg--I-----------------------geegtdY

             50        60        70        80        90
LCA          iNASFImsYwkpevmIAaQGPLkeTIgDFWqMIfqrKvkvIVMLTELkhg
RPTPase α    vNASFIdGYrQkdsyIAsQGPLLHTIeDFWRMIWewKscsIVMLTELeer
RPTPase β    INASYIMGYYQSNEFIITQHPLLHTIKDFWRMIWDHNAQIVVMiPDgQnm
RPTPase γ    INASYIMGYYrSNEFIITQHPLpHTtKDFWRMIWDHNAQiiVMIPDnQsI

CON          iNAS-ImgYyqsnefI-tQ-PLIhTikDFWrMIwdh-naqiVMI--q--

             100       110       120       130       140
LCA          dQEiCAQYW geGkqtYGDIeVdLKdtdksstYTI RvfeIrhskrkdSRtv
RPTPase α    gQEkCAQYWPsdGIvsYGDItVeLKkeeeCESYTV RdIIvtntreNkSRqI
RPTPase β    A EDEFVYWPn     kDEpi      NCESFkVTLmaeehkCLSNEEkII
RPTPase γ    A EDEFVYWPs     reEsm      NCEaFtVTLiskdrICLSNEEqiI

CON          aE-e--qYWps-g--ygd--v-Ik--nces-tvt--e-r-cIsne-r-i

             150                      160       170       180
LCA          yQy                 qY   tnWsveqIP aepKeIISmIqvVkQKIpQk
RPTPase α    rQf                 HF   hgWPevgiP SdgKgmISiIaaV Qk  Qq
RPTase β     IQDFILEATQDDYVLEVRHFQCPKWPNPDsPISkTFELISVI            K
RPTase γ     IhDFILEATQDDYVLEVRHFQCPKWPNPDaPISsTFELInVI            K

CON          iqdfileatqddyvIevrhfqcpkWpnpd-Pis-t-eIIsvI-----------qk
```

FIG.5C

```
                    190         200       210       220       230
LCA           nsseGNkhhhkstPIIiHCrdGsqqTGiFCALInILEsaetEevvDiFQvVKa
                  ||       |   ||  |   || ||||   ||     |   | || ||
RPTPase α      qqsGNh      PitVHCsaGagrTGTFCALsTvLErvkaEgiIDVFQtVKs
                   |       |  ||   |    |||||| |       |   || |
RPTPase β      EEAaNR    DGPmIVHDEhGgVtAGTFCALTTLmhQLEkENsVDVyQVAKM
               |||  |    ||| ||||| | | ||   ||||||  ||| || ||| |||||
RPTPase γ      EEAItR    DGPtIVHDEyGaVsAGmICALTTLsqQLEnENaVDVfQVAKM

CON           -eea-nr----dgP-ivH-e-Gav--GtfCALttlleqle-En-vDvfQv-Km

                 240       250
LCA           LrkaRPgMVsTfEQYqFIYdVias
              |   || || | ||| | | |
RPTPase α     LaLqRPhMVqTIEQYeFcYKVvqe
                |  ||      ||| | |||
RPTPase β     INLMRPGVFaDIEQYQFIYKViLS
              ||||||||| |||||||  ||  ||
RPTPase γ     INLMRPGVFtDIEQYQFIYKarLS

CON           -nlmRPg----iEQYqFIYkvils
```

FIG.5D

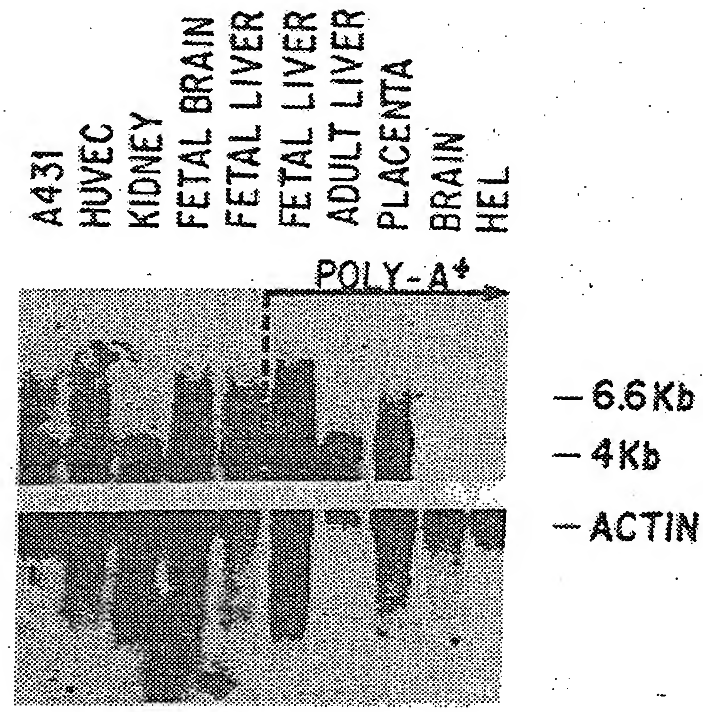
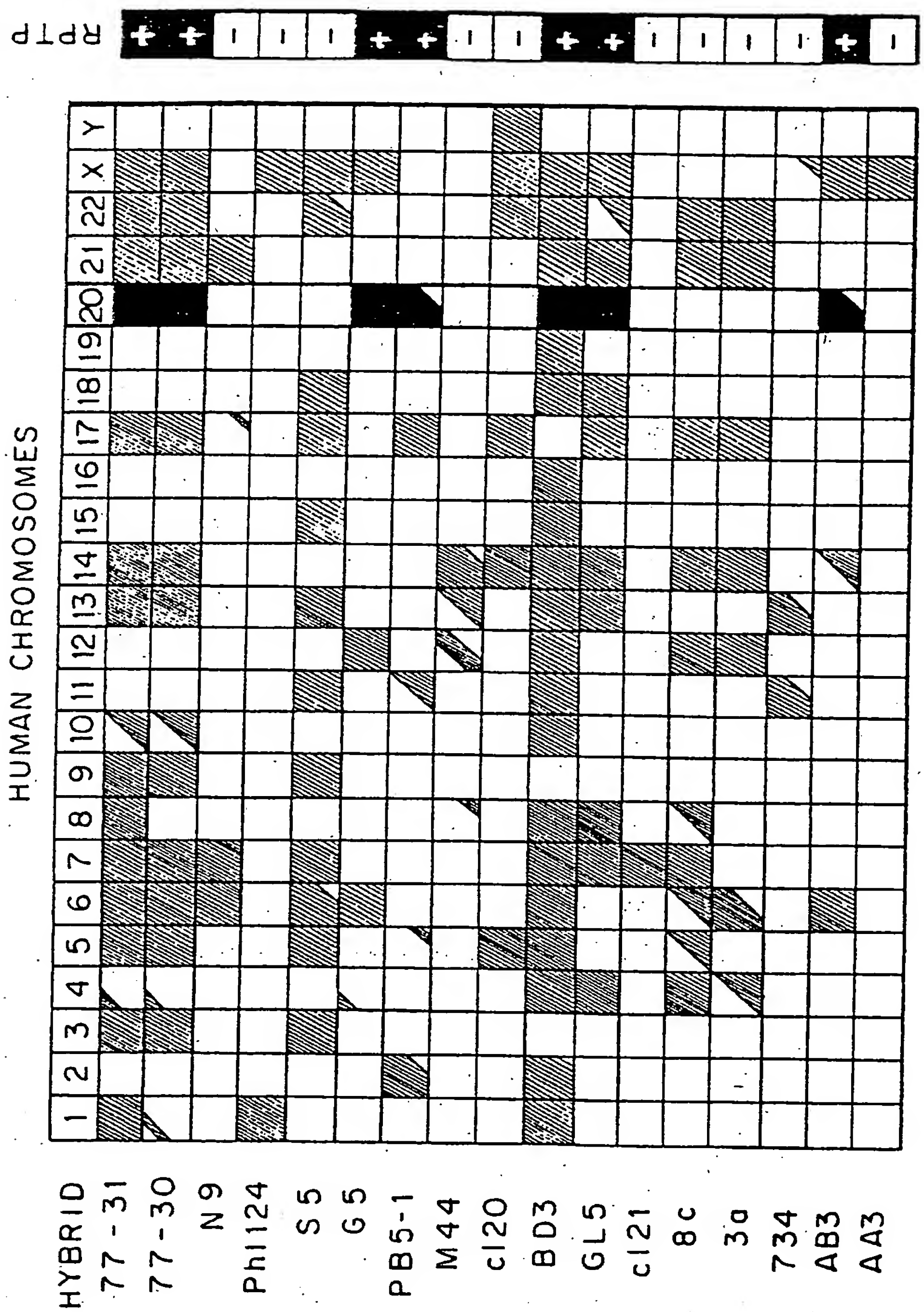

A431
HUVEC
KIDNEY
FETAL BRAIN
FETAL LIVER
FETAL LIVER
ADULT LIVER
PLACENTA
BRAIN
HEL
POLY-A+
6.6Kb
4Kb
ACTIN

FIG. 6

FIG. 7


RPTP α
HUMAN CHROMOSOMES
HYBRID
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
77-31
77-30
N9
Ph124
S5
G5
PB5-1
M44
cl20
BD3
GL5
cl21
8c
3a
734
AB3
AA3
+ + - - - + + - - + + - - - - + -

```
  1 ATGGATTCCTGGTTCATTCTTGTTCTGCTCGGCAGTGGTCTGATATGTGTCAGTGCCAAC  60
  1[M  D  S  W  F  I  L  V  L  L  G  S  G  L  I  C  V  S] A  N   20
   SIGNAL PEPTIDE

 61 AATGCTACCACAGTTGCACCTTCTGTAGGAATTACAAGATTAATTAACTCATCAACGGCA 120
 21 N  A  T  T  V  A  P  S  V  G  I  T  R  L  I  N  S  S  T  A   40

121 GAACCAGTTAAAGAAGAGGCCAAAACTTCAAATCCAACTTCTTCACTAACTTCTCTTTCT 180
 41 E  P  V  K  E  E  A  K  T  S  N  P  T  S  S  L  T  S  L  S   60

181 GTGGCACCAACATTCAGCCCAAATATAACTCTGGGACCCACCTATTTAACCACTGTCAAT 240
 61 V  A  P  T  F  S  P  N  I  T  L  G  P  T  Y  L  T  T  V  N   80

241 TCTTCAGACTCTGACAATGGGACCACAAGAACAGCAAGCACCAATTCTATAGGCATTACA 300
 81 S  S  D  S  D  N  G  T  T  R  T  A  S  T  N  S  I  G  I  T  100

301 ATTTCACCAAATGGAACGTGGCTTCCAGATAACCAGTTCACGGATGCCAGAACAGAACCC 360
101 I  S  P  N  G  T  W  L  P  D  N  Q  F  T  D  A  R  T  E  P  120

361 TGGGAGGGGAATTCCAGCACCGCAGCAACCACTCCAGAAACTTTCCCTCCTTCAGGTAAT 420
121 W  E  G  N  S  S  T  A  A  T  T  P  E  T  F  P  P  S  G  N  140

421 TCTGACTCGAAGGACAGAAGAGATGAGACACCAATTATTGCGGTGATGGTGGCCCTGTCC 480
141 S  D  S  K  D  R  R  D  E  T [P  I  I  A  V  M  V  A  L  S  160
                                  TRANSMEMBRANE SEGMENT
481 TCTCTGCTAGTGATCGTGTTTATTATCATAGTTTTGTACATGTTAAGGTTTAAGAAATAC 540
161 S  L  L  V  I  V  F  I  I  I  V  L  Y  M  L] R  F  K  K  Y  180

541 AAGCAAGCTGGGAGCCATTCCAATTCTTTCCGCTTATCCAACGGCCGCACTGAGGATGTG 600
181 K  Q  A  G  S  H  S  N  S  F  R  L  S  N  G  R  T  E  D  V  200

601 GAGCCCCAGAGTGTGCCACTTCTGGCCAGATCCCCAAGCACCAACAGGAAATACCCACCC 660
201 E  P  Q  S  V  P  L  L  A  R  S  P  S  T  N  R  K  Y  P  P  220

661 CTGCCCGTGGACAAGCTGGAAGAGGAAATTAACCGGAGAATGGCAGACGACAATAAGCTC 720
221 L  P  V  D  K  L  E  E  E  I  N  R  R  M  A  D  D  N  K  L  240

721 TTCAGGGAGGAATTCAACGCTCTCCCTGCATGTCCTATCCAGGCCACCTGTGAGGCTGCT 780
241 F  R  E  E  F  N  A  L  P  A  C  P  I  Q  A  T  C  E  A  A  260

781 TCCAAGGAGGAAAACAAGGAAAAAAATCGATATGTAAACATCTTGCCTTATGACCACTCT 840
261 S  K  E  E [N  K  E  K  N  R  Y  V  N  I  L  P  Y  D  H  S  280
              PTPase DOMAIN I
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FIG.8A

841 AGAGTCCACCTGACACCGGTTGAAGGGGTTCCAGATTCTGATTACATCAATGCTTCATTC 900
281 R V H L T P V E G V P D S D Y I N A S F 300

901 ATCAACGGTTACCAAGAAAAGAACAAATTCATTGCTGCACAAGGACCAAAAGAAGAAACG 960
301 I N G Y Q E K N K F I A A Q G P K E E T 320

961 GTGAATGATTTCTGGCGGATGATCTGGGAACAAAACACAGCCACCATCGTCATGGTTACC 1020
321 V N D F W R M I W E Q N T A T I V M V T 340

1021 AACCTGAAGGAGAGAAAGGAGTGCAAGTGCGCCCAGTACTGGCCAGACCAAGGCTGCTGG 1080
341 N L K E R K E C K C A Q Y W P D Q G C W 360

1081 ACCTATGGGAATATTCGGGTGTCTGTAGAGGATGTGACTGTCCTGGTGGACTACACAGTA 1140
361 T Y G N I R V S V E D V T V L V D Y T V 380

1141 CGGAAGTTCTGCATCCAGCAGGTGGGCGACATGACCAACAGAAAGCCACAGCGCCTCATC 1200
381 R K F C I Q Q V G D M T N R K P Q R L I 400

1201 ACTCAGTTCCACTTTACCAGCTGGCCAGACTTTGGGGTGCCTTTTACCCCGATCGGCATG 1260
401 T Q F H F T S W P D F G V P F T P I G M 420

1261 CTCAAGTTCCTCAAGAAGGTGAAGGCCTGTAACCCTCAGTATGCAGGGGCCATCGTGGTC 1320
421 L K F L K K V K A C N P Q Y A G A I V V 440

1321 CACTGCAGTGCAGGTGTAGGGCGTACAGGTACCTTTGTCGTCATTGATGCCATGCTGGAC 1380
441 H C S A G V G R T G T F V V I D A M L D 460

1381 ATGATGCATACAGAACGGAAGGTGGACGTGTATGGCTTTGTGAGCCGGATCCGGGCACAG 1440
461 M M H T E R K V D V Y G F V S R I R A Q 480

1441 CGCTGCCAGATGGTGCAAACCGATATGCAGTATGTCTTCATATACCAAGCCCTTCTGGAG 1500
481 R C Q M V Q T D M Q Y V F I Y Q A L L E] 500

1501 CATTATCTCTATGGAGATACAGAACTGGAAGTGACCTCTCTAGAAACCCACCTGCAGAAA 1560
501 H Y L Y G D T E L E V T S L E T H L Q K 520

1561 ATTTACAACAAAATCCCAGGGACCAGCAACAATGGATTAGAGGAGGAGTTTAAGAAGTTA 1620
521 I Y N K I P G T S N N G L E E E F K K L 540

FIG.8B

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1621 ACATCAATCAAAATCCAGAATGACAAGATGCGGACTGGAAACCTTCCAGCCAACATGAAG 1680
 541 T  S  I  K  I  Q  N  D  K  M  R  T  G  N  L  P  A [N  M  K   560
                                                      PTPase Domain II
1681 AAGAACCGTGTTTTACAGATCATTCCATATGAATTCAACAGAGTGATCATTCCAGTTAAG 1740
 561 K  N  R  V  L  Q  I  I  P  Y  E  F  N  R  V  I  I  P  V  K   580

1741 CGGGGCGAAGAGAATACAGACTATGTGAACGCATCCTTTATTGATGGCTACCGGCAGAAG 1800
 581 R  G  E  E  N  T  D  Y  V  N  A  S  F  I  D  G  Y  R  Q  K   600

1801 GACTCCTATATCGCCAGCCAGGGCCCTCTTCTCCACACAATTGAGGACTTCTGGCGAATG 1860
 601 D  S  Y  I  A  S  Q  G  P  L  L  H  T  I  E  D  F  W  R  M   620

1861 ATCTGGGAGTGGAAATCCTGCTCTATCGTGATGCTAACAGAACTGGAGGAGAGAGGCCAG 1920
 621 I  W  E  W  K  S  C  S  I  V  M  L  T  E  L  E  E  R  G  Q   640

1921 GAGAAGTGTGCCCAGTACTGGCCATCTGATGGACTGGTGTCCTATGGAGATATTACAGTG 1980
 641 E  K  C  A  Q  Y  W  P  S  D  G  L  V  S  Y  G  D  I  T  V   660

1981 GAACTGAAGAAGGAGGAGGAATGTGAGAGCTACACCGTCCGAGACCTCCTGGTCACCAAC 2040
 661 E  L  K  K  E  E  E  C  E  S  Y  T  V  R  D  L  L  V  T  N   680

2041 ACCAGGGAGAATAAGAGCCGGCAGATCCGGCAGTTCCACTTCCATGGCTGGCCTGAAGTG 2100
 681 T  R  E  N  K  S  R  Q  I  R  Q  F  H  F  H  G  W  P  E  V   700

2101 GGCATCCCCAGTGACGGAAAGGGCATGATCAGCATCATCGCCGCCGTGCAGAAGCAGCAG 2160
 701 G  I  P  S  D  G  K  G  M  I  S  I  I  A  A  V  Q  K  Q  Q   720

2161 CAGCAGTCAGGGAACCACCCCATCACCGTGCACTGCAGCGCCGGGGCAGGAAGGACGGGG 2220
 721 Q  Q  S  G  N  H  P  I  T  V  H  C  S  A  G  A  G  R  T  G   740

2221 ACCTTCTGTGCCCTGAGCACCGTCCTGGAGCGTGTGAAAGCAGAGGGGATTTTGGATGTC 2280
 741 T  F  C  A  L  S  T  V  L  E  R  V  K  A  E  G  I  L  D  V   760

2281 TTCCAGACTGTCAAGAGCCTGCGGCTACAGAGGCCACACATGGTCCAGACACTGGAACAG 2340
 761 F  Q  T  V  K  S  L  R  L  Q  R  P  H  M  V  Q  T  L  E  Q   780

2341 TATGAGTTCTGCTACAAGGTGGTGCAGGAGTATATTGATGCATTCTCAGATTATGCCAAC 2400
 781 Y  E  F  C  Y  K  V  V  Q  E] Y  I  D  A  F  S  D  Y  A  N   800

2401 TTCAAGTAA 2409
 801 F  K  *  803
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FIG.8C